## **AMENDMENTS TO THE SPECIFICATION**

Please amend the specification as follows:

Please amend Table 1 spanning pages 7-8, by increasing the line spacing from single-line spacing to 1½-line spacing, as shown below:

Table 1

| Amino AcidAbbreviationAlanineAArginineRAsparagineNAspartic AcidDCysteineCGlutamineQ | Three-Letter<br>Abbreviation |
|---|------------------------------|
| Asparagine N Aspartic Acid D Cysteine C   | Ala                          |
| Aspartic Acid D Cysteine C  | Arg                          |
| Cysteine C  | Asn                          |
|   | Asp                          |
| Glutamine Q   | Cys                          |
|   | Gln                          |
| Glutamic Acid E   | Glu                          |
| Glycine G   | Gly                          |
| Histidine H   | His                          |
| Isoleucine I  | Ile                          |
| Leucine L   | Leu                          |
| Lysine K  | Lys                          |
| Methionine M  | Met                          |
| Phenylalanine F   | Phe                          |
| Proline P   | Pro                          |
| Serine S  | Ser                          |
| Threonine T   | Thr                          |
| Tryptophan W  | Trp                          |
| Tyrosine Y  |                              |
| Valine V  | Tyr                          |

Please amend Table 2, beginning on page 18, line 13, by increasing the line spacing from single-line spacing to 1½-line spacing, as shown below (no additions or deletions to the amino acid sequences are to be made to Table 2):

## Table 2

| Amino    | Acid  | Seo | uences  | of Edg | Receptors  |
|----------|-------|-----|---------|--------|------------|
| ZNIHILIO | riciu | DUG | uclices | VILLUZ | ixeceptors |

| •               | MGPTSVPLVKAHRSSVSDYVNYDIIVRHYNYTGKLNISAD   |
|-----------------|--|
| Human Edg 1     | KENSIKLTSVVFILICCFIILENIFVLLTIWKTKKFHRPM   |
| (SEQ ID NO: 1)  | YYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLR   |
|                 | EGSMFVALSASVFSLLAIAI ERYITMLKMKLHNGSNNFRL  |
| Genbank         | FLLISACWVISLILGGLPIMGWNCISALSSCSTVLPLYHK   |
| Accession No.   | HYILFCTTVFTLLLLSIVILYCRIYSLVRTRSRRLTFRKN   |
| AF233365        | ISKASRSSEKSLALLKTVIIVLSVFIACWAPLFILLLLDV   |
|                 | GCKVKTCDILFRAEYFLVLAVLNSGTNPIIYTLTNKEMRR   |
|                 | AFIRIMSCCKCPSGDSAGKFKRPIIAGMEFSRSKSDNSSH   |
|                 | PQKDEGDNPETIMSSGNVNSSS   |
| II              | MARI COUCTOUR GODODON NOTO O CONTROL |
| Human Edg 2     | MAAISTSIPVISQPQFTAMNEPQCFYNESIAFFYNRSGKH   |
| (SEQ ID NO: 30) | LATEWNTVSKLVMGLGITVCIFIMLANLLVMVAI YVNRRF  |
|                 | HFPIYYLMANLAAADFFAGLAYFYLMFNTGPNTRRLTVST   |
| Genbank         | WLLRQGLIDTSLTASVANLLAIAI ERHITVFRMQLHTRMS  |
| Accession       | NRRVVVVIVVIWTMAIVMGAIPSVGWNCICDIENCSNMAP   |
| No. U78192      | LYSDSYLVFWAIFNLVTFVVMVVLYAHIFGYVRQRTMRMS   |
|                 | RHSSGPRRNRDTMMSLLKTVVIVLGAFIICWTPGLVLLLL   |
|                 | <u>D</u> VCCPQCDVLAY <u>EKFFLLLAEFNSAMNPIIYSYRDKEMSA</u>   |
|                 | TFRQILCCQRSENPTGPTEGSDRSASSLNHTILAGVHSND   |
|                 | HSVV   |
|                 |  |
| Human Edg 3     | ${\tt MATALPPRLQPVRGNETLREHYQYVGKLAGRLKEASEGS\underline{T}}$   |
| (SEQ ID NO: 2)  | LTTVLFLVICSFIVLENLMVLIAI WKNNKFHNRMYFFIGN  |
|                 | LALCDLLAGIAYKVNILMSGKKTFSLSPTVWFLREGSMFV   |
| Genbank         | ALGASTCSLLAIAI ERHLTMIKMRPYDANKRHRVFLLIGM  |
|                 |  |

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Accession No. CWLIAFTLGALPILGWNCLHNLPDCSTILPLYSKKYIAFC

X83864 ISIFTAILVTIVILYARIYFLV*KSSSRKVANHNNSERSMA* 

LLRTVVIVVSVFIACWSPLFILFLIDVACRVQACPILFKA

QWFIVLAVLNSAMNPVIYTLASKEMRRAFFRLVCNCLVRG

RGARASPIQPALDPSRSKSSSSNNSSHSPKVKEDLPHTDP

*SSCIMDKNAALQNGIFCN* 

Human Edg 4 MVIMGQCYYNETIGFFYNNSGKELSSHWRPKDVVVVALGL

(SEQ 1D NO: 31) TVSVLVLLTNLLVIAAIASNRRFHQPIYYLLGNLAAADLF

AGVAYLFLMFHTGPRTARLSLEGWFLRQGLLDTSLTASVA

Genbank TLLAIAV*ERHRSVMAVQLHSRLPRG*RVVMLIVGVWVAALG

Accession No. LGLLPAHSWHCLCALDRCSRMAPLLSRSYLAVWALSSLLV

AF233092 FLLMVAVYTRIFFYVRRRVQRMAEHVSCHPRYRETTLSLV

KTVVIILGAFVVCWTPGQVVLLLDGLGCESCNVLAVEKYF

LLLAEANSLVNAAVYSCRDAEMRRTFRRLLCCACLRQSTR

*ESVHYTSSAQGGASTRIMLPENGHPLMDSTL* 

Human Edg 4 mt MVIMGQCYYNETIGFFYNNSGKELSSHWRPKDVVVVALGL

(SEQ ID NO:32) TVSVLVLLTNLLVIAAIASNRRFHQPIYYLLGNLAAADLF

AGVAYLFLMFHTGPRTARLSLEGWFLRQGLLDTSLTASVA

Genbank TLLAIAVERHRSVMAVQLHSRLPRGRVVMLIVGVWVAALG

Accession No. LGLLPAHSWHCLCALDRCSRMAPLLSRSYLAVWALSSLLV

AF011466 FLLMVAVYTRI*FFYVRRRVQRM*AEHVSCHPRYRETTLSLV

KTVVIILGAFVVCWTPGQVVLLLDGLGCESCNVLAVEKYF

LLLAEANSLVNAAVYSCRDAEMRRTFRRLLCCACLRQSTR

ESVHYTSSAQGGASTRIMLPENGHPLMTPPFSYLELQRYA

ASNKSTAPDDLWVLLAQPNQQD

| Human Edg 5     | ${\tt MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFI}$   |
|-----------------|--|
| (SEQ ID NO: 33) | $\underline{\texttt{VILCCAIVVENLLVLIAV}} \underline{ARNSKFHS} \underline{\texttt{AMYLFLGNLAASDL}}$ |
|                 | <u>LAGVAFVANTLL</u> SGSVTLRLTPVQWFAREGSASITLSASV   |
| Genbank         | FSLLAIAI ERHVAIAKVKLYGSDKSCRMLLLIGASWLISL  |
| Accession No.   | <u>VLGGLPILGWNC</u> LGHLEACSTVLPLYAKHYVLCVVTIFSI   |
| AF034780        | <u>ILLAIVALYVRIYCVV</u> RSSHADMAAPQTLALLKTVTIVLG   |
|                 | <u>VFIVCWLPAFSILLLD</u> YACPVHSCPILYKAHYFFAVSTLN   |
|                 | <u>SLLNPVIYTW</u> RSRDLRREVLRPLQCWRPGVGVQGRRRVGT   |
|                 |  |

PGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV

| Human Edg 6     | MNATGTPVAPESCQQLAAGGHSRLIVLHYNHSGRLAGRGG   |
|-----------------|--|
| (SEQ ID NO: 34) | ${\tt PEDGGL} \underline{{\tt GALRGLSVAASCLVVLENLLVLAAI}} \ \underline{{\tt TSHMRSRRW}}$ |
| Genbank         | $\underline{\text{VYYCLVNITLSDLLTGAAYLANVLL}} \underline{SGARTFRLAPAQWFL}$               |
| Accession No.   | $\underline{\texttt{REGLLFTALAASTFSLLFTAG}} \textit{ERFATMVRPVAESGATKTS}$                |
| AJ000479        | RVYGFIGLCWLLAALLGMLPLLGWNCLCAFDRCSSLLPLY   |
|                 | SKRYILFCLVIFAGVLATIMGLYGAIFRLVQASGQKAPRP   |
|                 | AARRKARRLLKTVLMILLAFLVCWGPLFGLLLADVFGSNL   |
|                 | WAQEYLRGMDWILALAVLNSAVNPIIYSFRSREVCRAVLS   |
|                 | FLCCGCLRLGMRGPGDCLARAVEAHSGASTTDSSLRPRDS   |
|                 | FRGSRSLSFRMREPLSSISSVRSI   |

Human Edg 7 MNECHYDKHMDFFYNRSNTDTVDDWTGTKLVIVLCVGTFF

SEQ ID NO: 35) CLFIFFSNSLVIAAV*IKNRKFHF*PFYYLLANLAAADFFAG

Genbank IAYVFLMFNTGPVSKTLTVNRWFLRQGLLDSSLTASLTNL

Accession No. LVIAVERHMSIMRMRVHSNLTKKRVTLLILLVWAIAIFMG

AF127138 AVPTLGWNCLCNISACSSLAPIYSRSYLVFWTVSNLMAFL

IMVVVYLRIYVYV*KRKTNVLSPHTSGSISRRRTPMKLMK*T

VMTVLGAFVVCWTPGLVVLLLDGLNCRQCGVQHVKRWFLL

LALLNSVVNPIIYSYKDEDMYGTMKKMICCFSQENPERRP

SRIPSTVLSRSDTGSQYIEDSISQGAVCNKSTS

Human Edg 8 MESGLLRPAPVSEVIVLHYNYTGKLRGARYQPGAGLRADA

(SEQ ID NO: 36) VVCLAVCAFIVLENLAVLLVLGRHPRFHAPMFLLLGSLTL

Genbank SDLLAGAAYAANILLSGPLTLKLSPALWFAREGGVFVALT

Accession No. ASVLSLLAIALERSLTMARRGPAPVSSRGRTLAMAAAAWG

AF317676 VSLLLGLLPALGWNCLGRLDACSTVLPLYAKAYVLFCVLA

FVGILAAICALYARI*YCQVRANARRLPARPGTAGTTSTRA* 

RRKPRSLALLRTLSVVLLAFVACWGPLFLLLLLDVACPAR

TCPVLLQADPFLGLAMANSLLNPIIYTLTNRDLRHALLRL

*VCCGRHSCGRDPSGSQQSASAAEASGGLRRCLPPGLDGSF* 

SGSERSSPORDGLDTSGSTGSPGAPTAARTLVSEPAAD

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Please amend Table 3, beginning on page 21, line 1, by increasing the line spacing from single-line spacing to  $1\frac{1}{2}$ -line spacing, as shown below (no additions or deletions to the amino acid sequences are to be made to Table 3):

## Table 3

## **Amino Acid Sequences of Chimeric Edg Receptors**

Edg1/3(ct) MGPTSVPLVKAHRSSVSDYVNYDIIVRHYNYTGKLNISAD

KENSIKLTSVVFILICCFIILENIFVLLTIWKTKKFHRPM
YYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAOWFLR

EGSMFVALSASVFSLLAIA*IERYITMLKMKLHNGSNNF*RL

FLLISACWVISLILGGLPIMGWNCISALSSCSTVLPLYHK

HYILFCTTVFTLLLLSIVILYCRIYSLVRTRSRRLTFRKN

ISKASRSSEKSLALLKTVIIVLSVFIACWAPLFILLLLDV

GCKVKTCDILFRAEYFLVLAVLNSGTNPIIYTLTSKEMRR

AFFRLVCNCLVRGRGARASPIQPALDPSRSKSSSSNNSSH

SPKVKEDLPHTDPSSCIMDKNAALQNGIFCN

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(SEQ ID NO: 3)

Edgl/3(i3ct)

(SEQ ID NO: 4)

MGPTSVPLVKAHRSSVSDYVNYDIIVRHYNYTGKLNISAD
KENSIKLTSVVFILICCFIILENIFVLLTIWKTKKFHRPM
YYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLR
EGSMFVALSASVFSLLAIAIERYITMLKMKLHNGSNNFRL
FLLISACWVISLILGGLPIMGWNCISALSSCSTVLPLYHK
HYILFCTTVFTLLLLSIVILYCRIYSLVRSSSRKVANHNN
SERSMALLRTVIIVLSVFIACWAPLFILLLLDVGCKVKTC
DILFRAEYFLVLAVLNSGTNPIIYTLTSKEMRRAFFRLVC
NCLVRGRGARASPIQPALDPSRSKSSSSNNSSHSPKVKED
LPHTDPSSCIMDKNAALQNGIFCN

Edgl/3(i2i3ct)

(SEQ ID NO:5)

MGPTSVPLVKAHRSSVSDYVNYDIIVRHYNYTGKLNISAD
KENSIKLTSVVFILICCFIILENIFVLLTIWKTKKFHRPM
YYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLR
EGSMFVALSASVFSLLAIAIERHLTMIKMRPYDANKRHRL
FLLISACWVISLILGGLPIMGWNCISALSSCSTVLPLYHK
HYILFCTTVFTLLLLSIVILYCRIYSLVRSSSRKVANHNN
SERSMALLRTVIIVLSVFIACWAPLFILLLLDVGCKVKTC
DILFRAEYFLVLAVLNSGTNPIIYTLTSKEMRRAFFRLVC
NCLVRGRGARASPIQPALDPSRSKSSSNNSSHSPKVKED
LPHTDPSSCIMDKNAALQNGIFCN

Edg 5/3(i3ct)

(SEQ ID NO:37)

MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFI VILCCAIVVENLLVLIAV*ARNSKFH*SAMYLFLGNLAASDL LAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISL
VLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSI
ILLAIVALYVRIYCVVKSSSRKVANHNNSERSMALLRTVT
IVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAV
STLNSLLNPVIYTWASKEMRRAFFRLVCNCLVRGRGARAS
PIQPALEPSRSKSSSSNNSSHSPKVKEDLPHTDPSSCIMD
KNAALQNGIFCN

Edg8/4(ct)

(SEQ ID NO: 38)

MESGLLRPAPVSEVIVLHYNYTGKLRGARYQPGAGLRADA
VVCLAVCAFIVLENLAVLLVLGRHPRFHAPMFLLLGSLTL
SDLLAGAAYAANILLSGPLTLKLSPALWFAREGGVFVALT
ASVLSLLAIALERSLTMARRGPAPVSSRGRTLAMAAAAWG
VSLLLGLLPALGWNCLGRLDACSTVLPLYAKAYVLFCVLA
FVGILAAICALYARIYCQVRANARRLPARPGTAGTTSTRA
RRKPRSLALLRTLSVVLLAFVACWGPLFLLLLLDVACPAR
TCPVLLQADPFLGLAMANSLLNPIIYTLRDAEMRRTFRRL
LCCACLRQSTRESVHYTSSAQGGASTRIMLPENGHPLMTP
PFSYLELQRYAASNKSTAPDDLWVLLAQPNOOD

Please amend Table 4, beginning on page 35, line 13, by increasing the line spacing from single-line spacing to 1½-line spacing, as shown below (no additions or deletions to the amino acid sequences are to be made to Table 4):

<u>Table 4</u>

<u>PCR Primers for Generating Chimeric Edg 1 Receptors</u>

| <u>Primer</u>   | Direction Pos | ition | Sequence 5'-3'   |
|-----------------|---------------|-------|--|
| Edg-1           |               | 1     | CCC/GCG/GTT/AAC/ATG/GGG/CCC/ACC/   |
| (SEQ ID NO: 6)  |               |       | AGC/GTC  |
|                 |               |       |  |
| Edg-3           | rev           | 1137  | CGC/GGA/TCC/TCA/GTT/GCA/GAA/GAT/   |
| (SEQ ID NO: 7)  |               |       | CCC  |
|                 |               |       |  |
| É1/3 CTD        |               | 942   | CAT/TTA/CAC/TCT/GAC/CAG/CAA/GGA/   |
| (SEQ ID NO: 8)  |               |       | GAT/GCG/GCG/G  |
|                 |               |       |  |
| E1/3 CTD        | rev           | 942   | CCG/CAT/CTC/CTT/GCT/GGT/CAG/AGT/   |
| (SEQ ID NO: 9)  |               |       | GTA/AAT/GAT/G  |
|                 |               |       |  |
| E1/3 i2         |               | 402   | GTC/TCC/TCG/CCA/TCG/CCA/TCG/AGC/   |
| (SEQ ID NO: 10) |               |       | GGC/ACT/TGA/C  |
| 71/0:0          |               | 40.   |  |
| E1/3 i2         | rev           | 402   | GTC/AAG/TGC/CGC/TCG/ATG/GCG/ATG/   |
| (SEQ ID NO:11)  |               |       | GCG/AGG/AGA  |
| E1/2 :2         |               | 4.41  | 000/01 1/01 1/01 0/02 1/02 0/22 1/02 1/0 |
| E1/3 i2         |               | 441   | CGC/CAA/CAA/GAG/GCA/CCG/CCT/CTT/   |
| (SEQ ID NO:12)  |               |       | CCT/GCT/AAT/C  |

| E1/3 i2        | rev | 441 | GAT/TAG/CAG/GAA/GAG/GCG/GTG/CCT/ |
|----------------|-----|-----|----------------------------------|
| (SEQ ID NO:13) |     |     | CTT/GTT/GGC/G                    |
| E1/3 i3        |     | 684 | CTA/CTC/CTT/GGT/CAG/GTC/CAG/CAG/ |
| (SEQ ID NO:14) |     |     | CCG/TAA/GGT/G                    |
| E1/3 i3        | rev | 684 | CAC/CTT/ACG/GCT/GCT/GGA/CCT/GAC/ |
| (SEQ ID NO:15) |     |     | CAA/GGA/GTA/G                    |
| E1/3 i3        |     | 723 | CAC/TGC/TGC/GGA/CCG/TGA/TTA/TCG/ |
| (SEQ ID NO:16) |     |     | TCC/TGA/GCG/TC                   |
| E1/3 i3        | rev | 723 | GAC/GCT/CAG/GAC/GAT/AAT/CAC/GGT/ |
| (SEQ ID NO:17) |     |     | CCG/CAG/CAG/TG                   |

Please amend Table 5, beginning on page 38, line 1, by increasing the line spacing from single-line spacing to  $1\frac{1}{2}$ -line spacing, as shown below (no additions or deletions to the amino acid sequences are to be made to Table 5):

<u>Table 5</u>

<u>PCR Primers for Generating Chimeric Edg 5 Receptors</u>

| <u>Primer</u>  | <u>Direction</u> | Position | Sequence 5'-3'                |
|----------------|------------------|----------|-------------------------------|
| Edg-5          |                  | 1        | CCC/GCG/GTT/AAC/ATG/GGC/AGC/  |
| (SEQ ID NO:18) |                  |          | TTG/TAC/TCG                   |
| Edg-3          | rev              | 1137     | CGC/GGA/TCC/TCA/GTT/GCA/GAA/  |
| (SEQ ID NO:19) |                  |          | GAT/CCC                       |
| E5/3           |                  | 864      | CGT/CAT/CTA/CAC/GTG/GGC/CAG/  |
| (SEQ ID NO:20) |                  |          | CAA/GGA/GAT/GCG/G             |
| E5/3           | rev              | 864      | CCG/CAT/CTC/CTT/GCT/GGC/CCA/  |
| (SEQ ID NO:21) |                  |          | CGT/GTA/GAT/GAC/G             |
| E5/3 i3        |                  | 633      | CAT/CTA/C TG/CGT/GGT/CAA/GTC/ |
| (SEQ ID NO:22) |                  |          | CAG/CAG/CCG/TAA/G             |
| E5/3 i3        | rev              | 633      | CTT/ACG/GCT/GCT/GGA/CTT/GAC/  |
| (SEQ ID NO:23) |                  |          | CAC/GCA/GTA/GAT/G             |
| E5/3 i3        |                  | 723      | CAC/TGC/TGC/GGA/CCG/TGA/CCA/  |
| (SEQ ID NO:24) |                  |          | TCG/TGC/TAG/GCG/TC            |
| E1/3 i3        | rev              | 723      | GAC/GCC/TAG/CAC/GAT/GGT/CAC/  |
| (SEQ ID NO:25) |                  |          | GGT/CCG/CAG/CAG/TG            |

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Please amend Table 6, beginning on page 39, line 8, by increasing the line spacing from single-line spacing to 1½-line spacing, as shown below (no additions or deletions to the amino acid sequences are to be made to Table 6):

<u>Table 6</u>

<u>PCR Primers for Generating Chimeric Edg 8 Receptors</u>

| <b>Primer</b>  | <b>Direction</b> | <b>Position</b> | Sequence 5'-3'               |
|----------------|------------------|-----------------|------------------------------|
| Edg-8          |                  | 1               | CCC/GCG/GTT/AAC/ATG/GAG/TCG/ |
| (SEQ ID NO:26) |                  |                 | GGG/CTG/CTG                  |
|                |                  |                 |                              |
| Edg-4-mut      | rev              | 1149            | CGC/GGA/TCC/TCA/GTC/CTG/TTG/ |
| (SEQ ID NO:27) |                  |                 | GTT/GGG                      |
|                |                  |                 |                              |
| E8/4           |                  | 920             | CCA/TCA/TCT/ACA/CGC/TCC/GAG/ |
| (SEQ ID NO:28) |                  |                 | ATG/CTG/AGA/TGC/G            |
|                |                  |                 |                              |
| E8/4           | rev              | 920             | CGC/ATC/TCA/GCA/TCT/CGG/AGC/ |
| (SEQ ID NO:29) |                  |                 | GTG/TAG/ATG/ATG/G            |